

Supplementary Table S1. Clinical characteristics of nasopharyngeal carcinoma patients according to the high and low expression of VIRMA

Characteristics	No. of patients	Expression of VIRMA		P value
		Low, n (%)	High, n (%)	
Age				
≤45	82	46 (54.8)	36 (45.6)	0.274
>45	81	38 (45.2)	43 (54.4)	
Sex				
Male	121	62 (73.8)	59 (74.7)	1.000
Female	42	22 (26.2)	20 (25.3)	
VCA-IgA				
≤ 1:160	74	39 (46.4)	35 (44.3)	0.875
> 1:160	89	45 (53.6)	44 (55.7)	
EA-IgA				
≤ 1:20	87	45 (53.6)	42 (53.2)	1.000
> 1:20	76	39 (46.4)	37 (46.8)	
T Stage				
T1-T2	68	37 (44.0)	31 (39.2)	0.634
T3-T4	95	47 (56.0)	48 (60.8)	
N Stage				
N0-N1	101	54 (64.3)	45 (59.5)	0.628
N2-N3	62	30 (35.7)	32 (40.5)	
TNM Stage				
I-II	43	20 (23.8)	23 (29.1)	0.480
III-IV	120	64 (76.2)	56 (70.9)	
Locoregional failure				
Yes	22	7 (8.3)	15 (19.0)	0.065
No	141	77 (91.7)	64 (81.0)	
Distant metastasis				
Yes	22	6 (7.1)	17 (21.5)	0.012
No	139	78 (92.9)	62 (78.5)	
Death				
Yes	34	8 (9.5)	26 (32.9)	0.001
No	129	76 (90.5)	53 (67.1)	

VCA-IgA: viral capsid antigen immunoglobulin A; EA-IgA: early antigen immunoglobulin A. All patients were restaged according to the 8th edition of the AJCC Cancer Staging Manual. Bold values indicate $P < 0.05$, P value is determined by χ^2 and Fisher's exact tests.

Supplementary Table S2. The top 20 proteins found by mass spectrometry analysis in the E2F7 group

Protein	Score	Matched peptides
Transcription factor E2F7, E2F7	3632	113
Poly [ADP-ribose] polymerase 1, PARP1	1112	45
X-ray repair cross-complementing protein 6, XRCC6	955	32
X-ray repair cross-complementing protein 5, XRCC5	875	44
Plectin, PLEC	616	27
Transcription factor A, mitochondrial, TFAM	352	20
Ezrin, EZR	315	13
DNA ligase 3, LIG3	287	14
Serine/arginine-rich splicing factor 1, SRSF1	250	11
Clathrin heavy chain 1, CLTC	245	11
Putative elongation factor 1-alpha-like 3, EEF1A1P5	221	7
4F2 cell-surface antigen heavy chain, SLC3A2	212	6
Protein S100-A7, S100A7	207	6
Polyadenylate-binding protein 1, PABPC1	187	8
Moesin, MSN	185	10
Complement C4-A, C4A	175	3
Radixin, RDX	169	9
Core-binding factor subunit beta, CBFB	167	2
Sodium/potassium-transporting ATPase subunit alpha, ATP1A1	167	7
Heat shock protein beta-1, HSPB1	166	5

Supplementary Table S3. qRT-PCR primers used in this study

Gene	Sequence (5' to 3')
VIRMA-F	TGACCTTGCCTCACCAACTGCA
VIRMA-R	AGCAACCTGGTGGTTTGGCTAG
KAT3A-F	AGTAACGGCACAGCCTCTCAGT
KAT3A-R	CCTGTCGATACAGTGCTTCTAGG
E2F7-F	TCTGAACCCGACTGTCCCTCTT
E2F7-R	TTTGGCAGCCACATCCAGAGTG
ANAPC1-F	CAACATGGCAGCTCTAAGTCG
ANAPC1-R	AACTTTTGCCACATAGGTCA
TET2-F	GCTTACCGAGACGCTGAGGAAA
TET2-R	AGAGAAGGAGGCACCACAGGT
ZNF407-F	CCGCAATGAAAGACCACTACAGG
ZNF407-R	TGTGCTGTCTGCGATGCTTGGT
FOXO3B-F	AAGTGGCTGCTCTGCGCCTC
FOXO3B-R	AAGCCGGTGCCTCTGCCATCTT
MYO1E-F	CCACTACATTGCTGCATCAAGC
MYO1E-R	AGGCATAGCCAGCTCTTCTCAC
TNRC6C-F	CACCGTTGCTTGGTCCAGTTTC
TNRC6C-R	TGCTGTGCCATTATCCACCAGG
TJP1-F	GTCCAGAATCTCGGAAAAGTGCC
TJP1-R	CTTTCAGCGCACCATAACCAACC
DOPEY1-F	GTCCAAACCAGGGAAGAGTAGC
DOPEY1-R	CATCTCCCAACTGGTCCCACAA
OBSCN-F	CAGCTCCATTGTCAGGGTG CAT
OBSCN-R	GGACGTTGTTTCCATAGCACCAC
CLCN5-F	GTATCTGTAGCCTTTGGAGCACC
CLCN5-R	GGCAGCAAAGAATGAACGCCAC
E2F7-m ⁶ A-F	TGCTGTAAATGAACTGTGCTA

(for MeRIP-qPCR)

E2F7-m⁶A-R

TTCTCAAGCCCACAGTCAGG

(for MeRIP-qPCR)

IGF2BP2-F

GTTGGTGCCATCATCGGAAAGG

IGF2BP2-R

TGGATGGTGACAGGCTTCTCTG

ITGA2-F

TCGTGCACAGTTTTGAAGATG

ITGA2-R

TGGAACACTTCCTGTTGTTACC

ITGA5-F

GTCGGGGGCTTCAACTTAGAC

ITGA5-R

CCTGGCTGGCTGGTATTAGC

NTRK1-F

CACTAACAGCACATCTGGAGACC

NTRK1-R

TGAGCACAAGGAGCAGCGTAGA

GAPDH-F

TGATGACATCAAGAAGGTGG

GAPDH-R

TTGTCATACCAGGAAATGAGC

Supplementary Table S4. siRNA sequence used in this study

Name	Sequence (5' to 3')
si-VIRMA-1#-F	CCAUCAUCUUUAGACCUAATT
si-VIRMA-1#-R	UUAGGUCUAAAGAUGAUGGTT
si-VIRMA-2#-F	GCUGAUCACGUAUCAUCUUTT
si-VIRMA-2#-R	AAGAUGAUACGUGAUCAGCTT
si-KAT3A-1#-F	GCACAGCCGUUUACCAUGATT
si-KAT3A-1#-R	UCAUGGUAAACGGCUGUGCTT
si-KAT3A-2#-F	GCUCUAUAAUCGCAAGACATT
si-KAT3A-2#-R	UGUCUUGCGAUUAUAGAGCTT
si-E2F7-1#-F	GCAAAUGGCCUACCUCCAATT
si-E2F7-1#-R	UUGGAGGUAGGCCAUUUGCTT
si-E2F7-2#-F	GCAUCUGUCUUACCAGAAUTT
si-E2F7-2#-R	AUUCUGGUAAGACAGAUGCTT
si-IGF2BP2-1#-F	CAUGCCGCAUGAUUCUUGATT
si-IGF2BP2-1#-R	UCAAGAAUCAUGCGGCAUGTT
si-IGF2BP2-2#-F	AACAGGGACCAAGAUAAACATT
si-IGF2BP2-2#-R	UGUUAUCUUGGUCCCUGUUTT
si-CBFB-F	CAGGAACCAAUCUGUCUCUTT
si-CBFB-R	AGAGACAGAUUGGUUCCUGTT

si-RUNX1-F

GGCAGAAACUAGAUGAUCATT

si-RUNX1-R

UGAUCAUCUAGUUUCUGCCTT

Supplementary Table S5. Primers used for shRNA plasmid construction

Name	Sequence (5' to 3')
sh-VIRMA-1#-F	CCGGTCGCCAACCTATCGCCTTAAACTCGAGTTTAA GGCGATAGGTTGGCGATTTTTTTG
sh-VIRMA-1#-R	AATTCAAAAATCGCCAACCTATCGCCTTAAACTCGA GTTTAAGGCGATAGGTTGGCGA
sh-VIRMA-2#-F	CCGGTACGCTCCTTTACACGATAAACTCGAGTTTATC GTGTAAAGGAGCGTATTTTTTTG
sh-VIRMA-2#-R	AATTCAAAAATACGCTCCTTTACACGATAAACTCGAG TTTATCGTGTAAGGAGCGTA
sh-VIRMA-3#-F	CCGGAGGAGTGATCAGTGGATTATTCTCGAGAATAAT CCACTGATCACTCCTTTTTTTTG
sh-VIRMA-3#-R	AATTCAAAAAGGAGTGATCAGTGGATTATTCTCGA GAATAATCCACTGATCACTCCT

Supplementary Table S6. Primers sequence used for ChIP-PCR assay

Name	Sequence (5' to 3')
VIRMA-ChIP-F1	ATTACTTCTGTCAATGGCACT
VIRMA-ChIP-R1	GTCTAAATGGCACAAACCCTT
VIRMA-ChIP-F2	GGTTCATTCTTCGTACCTGCT
VIRMA-ChIP-R2	GCAGGAAACATAAGTGCCAT
VIRMA-ChIP-F3	TTAGACTACCAAACCCGCTGA
VIRMA-ChIP-R3	ATTGTGTAACGTGAAGTACCAT
VIRMA-ChIP-F4	TGTTTCCTGCTCTTTTGCAAC
VIRMA-ChIP-R4	TGGAGCAACGAGATAAACTCA
ITGA2-ChIP-F	GGAGCCGGGCGCTGCCAA
ITGA2-ChIP-R	ACTCCGCCCCCGCAGCCTG
ITGA5-ChIP-F	TCCTCACTCACCCGTCTGTTCCC
ITGA5-ChIP-R	AGGCCCCAGCAGTACTCTCG
NTRK1-ChIP-F	TTCCCTTTCTCTGCCCCGTCT
NTRK1-ChIP-R	AGGACTACCAAAGGATCAATCGC

Supplementary Table S7. Probe sequence of E2F7 RNA pulldown assays

Name	Sequence (5' to 3')
E2F7-pulldown-1	GUAUAGUUUGGCGACUUA AUGCACC-Biotin
E2F7-pulldown-2	AGCUGCAUUCUCUUAGUAGGACCAC-Biotin
E2F7-pulldown-3	AUAGAUGCGUCUCCUUUCCACACCA-Biotin
E2F7-pulldown-4	UAAAGAGUAGCCACCUGAUCCUUGU-Biotin

Supplementary Table S8. Probe sequence of E2F7 *in situ* hybridization (ISH)

Name	Sequence (5' to 3')
E2F7-ISH-1	UUCUAAAGAGUAGCCACCUGAUCC-DIG*(Biotin)
E2F7-ISH-2	AAUCUGUAAAUGCAUCGUCCUUGU-DIG(Biotin)
E2F7-ISH-3	ACUGUGUAAAAAGAACCAUGGCGA-DIG(Biotin)
E2F7-ISH-4	GCCAUACUGAUUCUUAGCCACCCG-DIG(Biotin)

*DIG: digoxin